

0283

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OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/017,216

DATE: 01/10/2002  
 TIME: 14:49:23

Input Set : A:\10147571.app  
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3 <110> APPLICANT: KAPPELLER-LIBERMANN, Rosana  
 5 <120> TITLE OF INVENTION: 13245, A Novel Human Myotonic Dystrophy Type Protein  
 6 Kinase and Uses Therefor  
 8 <130> FILE REFERENCE: 10147-57U1  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/017,216  
 11 <141> CURRENT FILING DATE: 2001-10-23  
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,429  
 14 <151> PRIOR FILING DATE: 2000-10-23  
 16 <160> NUMBER OF SEQ ID NOS: 7  
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 29 ctctttgttc tctttgaaga atgcagtcag cctgctctga tgaagattaa gcacgtgagc 240  
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141 &lt;213&gt; ORGANISM: Homo sapiens

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150 Gly Lys Pro Pro Phe Met Thr Gln Gln Gln Met Ser Pro Leu Ser Arg
151 35 40 45
153 Glu Gly Ile Leu Asp Ala Leu Phe Val Leu Phe Glu Glu Cys Ser Gln
154 50 55 60
156 Pro Ala Leu Met Lys Ile Lys His Val Ser Asn Phe Val Arg Lys Tyr
157 65 70 75 80
159 Ser Asp Thr Ile Ala Glu Leu Gln Glu Leu Gln Pro Ser Ala Lys Asp
160 85 90 95
162 Phe Glu Val Arg Ser Leu Val Gly Cys Gly His Phe Ala Glu Val Gln
163 100 105 110
165 Val Val Arg Glu Lys Ala Thr Gly Asp Ile Tyr Ala Met Lys Val Met

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171 Glu Arg Asn Ile Leu Ser Arg Ser Thr Ser Pro Trp Ile Pro Gln Leu
172 145          150          155          160
174 Gln Tyr Ala Phe Gln Asp Lys Asn His Leu Tyr Leu Met Glu Glu Tyr
175          165          170          175
177 Gln Pro Gly Gly Asp Leu Leu Ser Leu Leu Asn Arg Tyr Glu Asp Gln
178          180          185          190
180 Leu Asp Glu Asn Leu Ile Gln Phe Tyr Leu Ala Glu Leu Ile Leu Ala
181          195          200          205
183 Val His Ser Val His Leu Met Gly Tyr Val His Arg Asp Ile Lys Pro
184          210          215          220
186 Glu Asn Ile Leu Val Asp Arg Thr Gly His Ile Lys Leu Val Asp Phe
187 225          230          235          240
189 Gly Ser Ala Ala Lys Met Asn Ser Asn Lys Met Val Asn Ala Lys Leu
190          245          250          255
192 Pro Ile Gly Thr Pro Asp Tyr Met Ala Pro Glu Val Leu Thr Val Met
193          260          265          270
195 Asn Gly Asp Gly Lys Gly Thr Tyr Gly Leu Asp Cys Asp Trp Trp Ser
196          275          280          285
198 Val Gly Val Ile Ala Tyr Glu Met Ile Tyr Gly Arg Ser Pro Phe Ala
199          290          295          300
201 Glu Gly Thr Ser Ala Arg Thr Phe Asn Asn Ile Met Asn Phe Gln Arg
202 305          310          315          320
204 Phe Leu Lys Phe Pro Asp Asp Pro Lys Val Ser Ser Asp Phe Leu Asp
205          325          330          335
207 Leu Ile Gln Ser Leu Leu Cys Gly Gln Lys Glu Arg Leu Lys Phe Glu
208          340          345          350
210 Gly Leu Cys Cys His Pro Phe Phe Ser Lys Ile Asp Trp Asn Asn Ile
211          355          360          365
213 Arg Asn Ser Pro Pro Pro Phe Val Pro Thr Leu Lys Ser Asp Asp Asp
214          370          375          380
216 Thr Ser Asn Phe Asp Glu Pro Glu Lys Asn Ser Trp Val Ser Ser Ser
217 385          390          395          400
219 Pro Cys Gln Leu Ser Pro Ser Gly Phe Ser Gly Glu Glu Leu Pro Phe
220          405          410          415
222 Val Gly Phe Ser Tyr Ser Lys Ala Leu Gly Ile Leu Gly Arg Ser Glu
223          420          425          430
225 Ser Val Val Ser Gly Leu Asp Ser Pro Ala Lys Thr Ser Ser Met Glu
226          435          440          445
228 Lys Lys Leu Leu Ile Lys Ser Lys Glu Leu Gln Asp Ser Gln Asp Lys
229          450          455          460
231 Cys His Lys Met Glu Gln Glu Met Thr Arg Leu His Arg Arg Val Ser
232 465          470          475          480
234 Glu Val Glu Ala Val Leu Ser Gln Lys Glu Val Glu Leu Lys Ala Ser
235          485          490          495
237 Glu Thr Gln Arg Ser Leu Leu Glu Gln Asp Leu Ala Thr Tyr Ile Thr
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246 Gln Ser Arg Lys Leu Gln Ile Lys Glu Gln Glu Tyr Gln Ala Gln
247 545          550          555          560
249 Val Glu Glu Met Arg Leu Met Met Asn Gln Leu Glu Glu Asp Leu Val
250          565          570          575
252 Ser Ala Arg Arg Arg Ser Asp Leu Tyr Glu Ser Glu Leu Arg Glu Ser
253          580          585          590
255 Arg Leu Ala Ala Glu Glu Phe Lys Arg Lys Ala Thr Glu Cys Gln His
256          595          600          605
258 Lys Leu Leu Lys Ala Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr
259          610          615          620
261 Ala Lys Leu Glu Lys Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu
262 625          630          635          640
264 Leu Gln Glu Lys Leu Glu Lys Ala Ala Lys Glu Arg Ala Glu Arg Glu
265          645          650          655
267 Leu Glu Lys Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys
268          660          665          670
270 Lys Leu Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val
271          675          680          685
273 Lys Arg Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp
274          690          695          700
276 Ile Gln Thr Lys Ser Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu
277 705          710          715          720
279 Glu Leu Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu
280          725          730          735
282 Glu Val His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys
283          740          745          750
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286          755          760          765
288 Glu Asn Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys
289          770          775          780
291 Ile Leu Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile
292 785          790          795          800
294 Arg Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala Asn Lys Leu
295          805          810          815
297 Ala Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys Ala Gln Glu
298          820          825          830
300 Glu Met Ile Ser Glu Leu Arg Gln Gln Lys Phe Tyr Leu Glu Thr Gln
301          835          840          845
303 Ala Gly Lys Leu Glu Ala Gln Asn Arg Lys Leu Glu Glu Gln Leu Glu
304          850          855          860
306 Lys Ile Ser His Gln Asp His Ser Asp Lys Asn Arg Leu Leu Glu Leu
307 865          870          875          880
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VERIFICATION SUMMARY

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